

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:39:01 ; Search time 585.791 Seconds
(without alignments)
11011.138 Million cell updates/sec

Title: US-09-856-681A-3
Perfect score: 216
Sequence: 1 ccgccgccgccgccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	216	100.0	495	12	BM855120	BM855120 K-EST0137	
2	216	100.0	496	9	AV704776	AV704776 AV704776	
3	216	100.0	815	13	BU850016	BU850016 AGENCOURT	
4	216	100.0	862	13	BQ723018	BQ723018 AGENCOURT	
5	216	100.0	928	10	BE898612	BE898612 601681550	
6	216	100.0	1013	10	BE899378	BE899378 601681309	
7	215	99.5	494	14	N31401	N31401 yx67d08.r1	
8	212.8	98.5	6875	11	BC032619	BC032619 Homo sapi	
9	212	98.1	462	14	N25829	N25829 yx22d01.r1	
10	203.6	94.3	410	14	N46020	N46020 yy35a05.r1	
11	193.6	89.6	632	14	CB577257	CB577257 AMGNNUC:C	
12	193.6	89.6	711	14	CB246380	CB246380 UI-M-FI0-	
13	193.6	89.6	2411	14	CB605722	CB605722 AMGNNUC:M	
c 14	178	82.4	291	10	BF702343	BF702343 MI-P-A2-a	
15	177.2	82.0	1183	12	BM546059	BM546059 AGENCOURT	
c 16	166.4	77.0	364	9	AA729933	AA729933 nx40f11.s	
17	166.2	76.9	628	9	AA625166	AA625166 af67e09.r	
18	161	74.5	304	9	AA369179	AA369179 EST80573	
19	161	74.5	624	10	AW957071	AW957071 EST369141	
20	159.6	73.9	486	10	BF775045	BF775045 285089 MA	
21	159.6	73.9	598	9	AV593974	AV593974 AV593974	
c 22	154	71.3	556	9	AA909230	AA909230 ol12h08.s	
c 23	141.8	65.6	342	14	CB693654	CB693654 AMGNNUC:C	
24	135.6	62.8	895	12	BI819955	BI819955 603035314	
25	117.6	54.4	841	13	BU390763	BU390763 603511251	
26	117.6	54.4	841	13	BU394026	BU394026 603802267	
c 27	110.6	51.2	1201	9	AL543312	AL543312 AL543312	
28	104.8	48.5	581	14	CB426060	CB426060 601199 MA	
29	104.8	48.5	852	10	BF306161	BF306161 601893009	
30	102.6	47.5	732	13	BQ180391	BQ180391 UI-M-EX0-	
31	99	45.8	543	12	BG698043	BG698043 602659189	
32	91.8	42.5	773	14	CF290712	CF290712 AGENCOURT	
33	90.2	41.8	566	12	BJ060286	BJ060286 BJ060286	
34	89.4	41.4	409	14	W92871	W92871 zd92h03.r1	
c 35	84.6	39.2	602	14	N22686	N22686 yx64c02.s1	
36	71.8	33.2	145	10	BG003350	BG003350 RC0-GN013	
37	62.8	29.1	829	12	BI824613	BI824613 603033546	
38	58.8	27.2	685	10	BE265000	BE265000 601193829	
c 39	58.4	27.0	589	14	CB426401	CB426401 601583 MA	
40	56	25.9	350	14	CD804283	CD804283 UI-M-GV0-	
c 41	55	25.5	420	10	BE709445	BE709445 IL3-HT061	
42	55	25.5	708	14	CD356790	CD356790 AGENCOURT	
43	55	25.5	740	12	BG571342	BG571342 602592610	
44	55	25.5	792	10	BE543221	BE543221 601069213	
45	55	25.5	3405	11	BC004330	BC004330 Homo sapi	

ALIGNMENTS

RESULT 1
BM855120
LOCUS BM855120 495 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0137909 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-150-D07
5', mRNA sequence.
ACCESSION BM855120
VERSION BM855120.1 GI:19211519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 495)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 150 row: D column: 07
High quality sequence stop: 495.
FEATURES Location/Qualifiers
source 1. .495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-150-D07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
ORIGIN

Query Match 100.0%; Score 216; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.8e-44;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      39 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 98

Qy     61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          |||
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Qy    121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db    159 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 218

Qy    181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db    219 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 254
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RESULT 2

AV704776

LOCUS AV704776 496 bp mRNA linear EST 09-OCT-2000

DEFINITION AV704776 ADB Homo sapiens cDNA clone ADBBJC04 5', mRNA sequence.

ACCESSION AV704776

VERSION AV704776.1 GI:10722088

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 496)

AUTHORS Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G.,
Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z.,
Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S.,
Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.

TITLE Homo sapiens cDNA ADB clones

JOURNAL Unpublished (2000)

COMMENT Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES Location/Qualifiers

source

1. .496

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ADBBJC04"

/tissue_type="Adrenal gland"

/dev_stage="Adult"

/lab_host="SOLR"

/clone_lib="ADB"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 496;
 Best Local Similarity 100.0%; Pred. No. 2.8e-44;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      181 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 240

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
          |||
Db      241 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 300

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      301 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 360

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      361 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 396
  
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RESULT 3

BU850016

LOCUS BU850016 815 bp mRNA linear EST 16-OCT-2002

DEFINITION AGENCOURT_10438272 NIH_MGC_109 Homo sapiens cDNA clone
 IMAGE:6598770 5', mRNA sequence.

ACCESSION BU850016

VERSION BU850016.1 GI:24034979

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 815)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM2832 row: b column: 18

High quality sequence stop: 700.

FEATURES Location/Qualifiers

source 1..815

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6598770"

/tissue_type="teratocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 815;
 Best Local Similarity 100.0%; Pred. No. 3.5e-44;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      96 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 155

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          |||
Db     156 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 215

Qy     121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db     216 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 275

Qy     181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db     276 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 311
  
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RESULT 4 BQ723018

LOCUS BQ723018 862 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT_8099701 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6190272 5', mRNA sequence.
 ACCESSION BQ723018
 VERSION BQ723018.1 GI:21861915
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 862)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM13588 row: n column: 01
High quality sequence stop: 592.

FEATURES
source Location/Qualifiers
1. .862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190272"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 862;
Best Local Similarity 100.0%; Pred. No. 3.6e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      269 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 328

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          |||
Db      329 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 388

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db      389 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 448

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      449 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 484
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RESULT 5 BE898612

LOCUS BE898612 928 bp mRNA linear EST 29-SEP-2000
DEFINITION 601681550F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951685 5',
mRNA sequence.
ACCESSION BE898612
VERSION BE898612.1 GI:10365266
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM820 row: c column: 14
High quality sequence stop: 794.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951685"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 216; DB 10; Length 928;
Best Local Similarity 100.0%; Pred. No. 3.7e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          |||
Db      303 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 362

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      363 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 422

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      423 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 458

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RESULT 6

BE899378
LOCUS BE899378 1013 bp mRNA linear EST 29-SEP-2000
DEFINITION 601681309F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951266 5',
mRNA sequence.
ACCESSION BE899378
VERSION BE899378.1 GI:10367019
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1013)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM819 row: b column: 03
High quality sequence start: 30
High quality sequence stop: 828.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951266"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 216; DB 10; Length 1013;
Best Local Similarity 100.0%; Pred. No. 3.9e-44;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      292 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 351

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TACTGACAAGGTCG 120
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Db      352 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TACTGACAAGGTCG 411

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Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
 |||
 Db 412 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 471
 Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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 Db 472 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 507

RESULT 7

N31401

LOCUS N31401 494 bp mRNA linear EST 10-JAN-1996

DEFINITION yx67d08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
 IMAGE:266799 5', mRNA sequence.

ACCESSION N31401

VERSION N31401.1 GI:1151800

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 494)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 464

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: T7

High quality sequence stop: 464.

FEATURES

source

Location/Qualifiers

1. .494

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3876441"

/db_xref="taxon:9606"

/clone="IMAGE:266799"

/sex="Male"

/tissue_type="melanocyte"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares melanocyte 2NbHM"

/note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGGAGCGCCGAGTTTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

```
Query Match          99.5%;  Score 215;  DB 14;  Length 494;
Best Local Similarity 99.5%;  Pred. No. 5e-44;
Matches 215;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGNC 119

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 179

Qy     121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 239

Qy     181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
        |||||||||||||||||||||||||||||||||||
Db     240 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 275
```

RESULT 8

BC032619

LOCUS BC032619 6875 bp mRNA linear HTC 04-MAR-2003

DEFINITION Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.

ACCESSION BC032619

VERSION BC032619.1 GI:22749800

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 6875)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 69 Row: o Column: 4

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 11991659

This clone has the following problem: retained intron.

FEATURES	Location/Qualifiers
source	1. .6875 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5578066" /tissue_type="Skin, melanotic melanoma." /clone_lib="NIH_MGC_72" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 98.5%; Score 212.8; DB 11; Length 6875;
Best Local Similarity 99.1%; Pred. No. 5.8e-43;
Matches 214; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60
Db	3666	CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCCGGTGCACAGCTCCCAGCCATCTGGC	3725
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG	120
Db	3726	CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG	3785
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC	180
Db	3786	GGGCTGTAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC	3845
Qy	181	CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA	216
Db	3846	CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA	3881

RESULT 9

N25829

LOCUS N25829 462 bp mRNA linear EST 29-DEC-1995

DEFINITION yx22d01.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:262465 5', mRNA sequence.

ACCESSION N25829

VERSION N25829.1 GI:1140177

KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 462)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 360
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1117 Std Error: 0.00
 Seq primer: T7
 High quality sequence stop: 360.

FEATURES Location/Qualifiers
 source 1. .462
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3872107"
 /db_xref="taxon:9606"
 /clone="IMAGE:262465"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NbHM"
 /note="Vector: pT7T3D (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGGAGCGCGCCGAGTTTTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 98.1%; Score 212; DB 14; Length 462;
 Best Local Similarity 98.1%; Pred. No. 2.8e-43;
 Matches 212; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 238 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 297

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120

```

|||||
Db      298 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCTACAANTCACTGACAAGGTCG 357
Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
|||||
Db      358 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCNTTTGNTCCC 417
Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db      418 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 453

```

RESULT 10

N46020

LOCUS N46020 410 bp mRNA linear EST 14-FEB-1996

DEFINITION yy35a05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:273200 5', mRNA sequence.

ACCESSION N46020

VERSION N46020.1 GI:1187186

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 410)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: T7

High quality sequence stop: 329.

FEATURES

source

Location/Qualifiers

1. .410

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3882842"

/db_xref="taxon:9606"

/clone="IMAGE:273200"

/sex="Male"

/tissue_type="melanocyte"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares melanocyte 2NbHM"

/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGAGTTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 94.3%; Score 203.6; DB 14; Length 410;
Best Local Similarity 98.1%; Pred. No. 3.5e-41;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      7 CCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
      || ||| |||||
Db      78 CCGCCCCACCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 137

Qy      67 GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG 126
      |||||
Db     138 GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG 197

Qy     127 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 186
      |||||
Db     198 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 257

Qy     187 ACATCCATGAAGCCCAATGATGCGTGTACA 216
      |||||
Db     258 ACATCCATGAAGCCCAATGATGCGTGTACA 287
```

RESULT 11

CB577257

LOCUS CB577257 632 bp mRNA linear EST 03-APR-2003

DEFINITION AMGNNUC:CDRG1-00015-G10-A cdrg1 (10898) Rattus norvegicus cDNA clone cdrg1-00015-g10 5', mRNA sequence.

ACCESSION CB577257

VERSION CB577257.1 GI:29521298

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 632)

AUTHORS Amgen EST Program.

TITLE Amgen Rat EST Program

JOURNAL Unpublished (2003)

COMMENT Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00015 row: g column: 10.

FEATURES Location/Qualifiers

source 1. .632

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="cdrg1-00015-g10"

/tissue_type="Chung Model Ipsilate"
/clone_lib="cdrg1 (10898)"
/note="Vector: pSPORT1; Chung Model Rat DRG Left L5/L6"

ORIGIN

Query Match 89.6%; Score 193.6; DB 14; Length 632;
Best Local Similarity 93.5%; Pred. No. 1.5e-38;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|| || |||||
Db 20 CCACCTCCCGCCCCGAGAGGGTGGACTCTATCCAGGTGCACAGCCCCAGCCCTCTGGC 79

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCTG 120
|||||
Db 80 CAGGCCGTGACTGTTTCGAGGCAGCCAGCCTCAATGCCTACAACCTCACTGACGAGGTCTG 139

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCTTTGCTCCC 180
|||||
Db 140 GGGCTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCCCCC 199

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 200 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 235

RESULT 12

CB246380

LOCUS CB246380 711 bp mRNA linear EST 09-JUL-2003

DEFINITION UI-M-F10-cdw-i-10-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE:6835379 5', mRNA sequence.

ACCESSION CB246380

VERSION CB246380.1 GI:28368024

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 711)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

The following repetitive elements were found in this cDNA

sequence: 563-665, >(CA)n#Simple_repeat

Seq primer: pYX-5.

FEATURES

Location/Qualifiers


```

source      1. .711
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6"
            /db_xref="taxon:10090"
            /clone="IMAGE:6835379"
            /tissue_type="whole brain"
            /dev_stage="embryo 12.5dpc"
            /lab_host="DH10B (T1 phage resistant)"
            /clone_lib="NIH_BMAP_F10"
            /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
            Site_2: Not I; The library was constructed according
            Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
            1996. Denatured RNA was size fractionated on a 1% agarose
            gel. First strand cDNA synthesis was primed with oligo-dT
            primer containing a Not I site. Double strand cDNA was
            size selected according to mRNA size fraction, ligated
            with EcoR I adaptor, digested with NotI and then cloned
            directionally into pYX-Asc vector. The library tag
            sequence located between the Not I site and the polyA tail
            is CAGCCACGAC. This library was created for the University
            Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
            Developing Mouse Nervous System', supported by National
            Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
            program coordinator."

```

ORIGIN

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Query Match      89.6%; Score 193.6; DB 14; Length 711;
Best Local Similarity 93.5%; Pred. No. 1.5e-38;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
        || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2 CCACCCCCCGCCCCGCAGCGGGTGGACTCTATCCAGGTGCACAGCTCCCAGCCCTCTGGC 61

Qy     61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     62 CAGGCCGTGACTGTTTCGAGGCAGCCAGCCTCAATGCCTACAACCTACTGACGAGGTCG 121

Qy    121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        ||||| || || ||||| ||||| || ||||| ||||| ||||| |||||
Db    122 GGGCTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCTCCC 181

Qy    181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    182 CTTTCCACATCCATGAAGCCCAATGATGCATGTACA 217

```

RESULT 13

```

CB605722
LOCUS      CB605722                2411 bp    mRNA    linear    EST 16-MAY-2003
DEFINITION AMGNNUC:MRPE3-00075-D4-WY placenta embryo D17 (10379) Rattus
            norvegicus cDNA clone mrpe3-00075-d4, mRNA sequence.
ACCESSION  CB605722
VERSION    CB605722.1  GI:29545334
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)

```

```

ORGANISM      Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Rattus.
REFERENCE     1 (bases 1 to 2411)
AUTHORS       Amgen EST Program.
TITLE         Amgen Rat EST Program
JOURNAL       Unpublished (2003)
COMMENT       Contact: Dan Fitzpatrick
               Amgen, Inc
               One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
               Tel: 805 447-4881
               Plate: 00075 row: d column: 4.
FEATURES             Location/Qualifiers
     source             1. .2411
                       /organism="Rattus norvegicus"
                       /mol_type="mRNA"
                       /db_xref="taxon:10116"
                       /clone="mrpe3-00075-d4"
                       /tissue_type="placenta embryo"
                       /clone_lib="placenta embryo D17 (10379)"
                       /note="Vector: pSPORT1; placenta embryo D17"
ORIGIN
Query Match      89.6%; Score 193.6; DB 14; Length 2411;
Best Local Similarity 93.5%; Pred. No. 2.6e-38;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy      1 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
      || || ||||||||||||||||||||||| ||||||||||||||| ||||||| |||||
Db     1340 CCACCTCCCGCCCCCGCAGAGGGTGGACTCTATCCAGGTGCACAGCCCCCAGCCCTCTGGC 1399

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
      ||||||||||||| ||||||||||||||| ||||||||||||||| |||||||
Db     1400 CAGGCCGTGACTGTTTCGAGGCAGCCCAGCCTCAATGCCTACAACCTCACTGACGAGGTCG 1459

Qy     121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
      ||||||||| || ||||||||||||| || ||||||||||||| ||||||| |||
Db     1460 GGGCTGAAGCGCACCCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCCCCC 1519

Qy     181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
      |||||||||||||||||||||||||||||
Db     1520 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1555

```

Qy	7	CCCCCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	66
Db	287	CCCC TTCGGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCGCAGCCCTCTGGCCAGGCC	228
Qy	67	GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TCACTGACAAGGTCGGGGCTG	126
Db	227	GTGACTGTTTCGAGGCAGCCAAGCCTCAATGCCTACAAC TCACTGACCAGGGCGGGGCTG	168
Qy	127	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCC	186
Db	167	AAACGCACCCCTTCGCTAAAGCCGGACGTGCCCCGAAACCTTCCTTTGCCCCCTTTCC	108
Qy	187	ACATCCATGAAGCCCAATGATGCGTGTACA	216

|||||
Db 107 ACATCCATGAAGCCCAATGACGCGTGTACA 78

RESULT 15

BM546059

LOCUS BM546059 1183 bp mRNA linear EST 20-FEB-2002

DEFINITION AGENCOURT_6497880 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588479
5', mRNA sequence.

ACCESSION BM546059

VERSION BM546059.1 GI:18778712

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1183)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12359 row: k column: 08

High quality sequence stop: 725.

FEATURES

Location/Qualifiers

source

1..1183

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5588479"

/lab_host="DH10B"

/clone_lib="NIH_MGC_125"

/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;

Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool

of three ovaries, from females ranging in age from 38 to

49 yo. Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 2.1 kb, insert size range 1-3.5 kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 036."

ORIGIN

Query Match 82.0%; Score 177.2; DB 12; Length 1183;

Best Local Similarity 97.2%; Pred. No. 2.7e-34;

Matches 212; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy 1 CCGCCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

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Db 741 CCGCCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 800

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Db      861 GGGGCTGAAGCGTACGCCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTC 920

Qy      179 CCCTTTCCACATCCATG-AAGCCCAATGATGCGTGTAC 215
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Db      921 CCCTTTTCACATCCATGAAAGCCCCATGATGCGTGTAC 958

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Search completed: March 26, 2004, 06:35:42
Job time : 590.791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 21:56:51 ; Search time 858.974 Seconds
(without alignments)
10899.164 Million cell updates/sec

Title: US-09-856-681A-3
Perfect score: 216
Sequence: 1 ccgccgccccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
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14: gb_vi:*
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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		8					Query	Description
Result	No.	Score	Match	Length	DB	ID		
	1	216	100.0	216	6	AX026743	AX026743	Sequence
	2	216	100.0	2123	6	AX876167	AX876167	Sequence
	3	216	100.0	2123	6	BD155987	BD155987	Primer fo
	4	216	100.0	2123	9	AK027439	AK027439	Homo sapi
	5	216	100.0	2227	6	BD127394	BD127394	Primer fo
	6	216	100.0	2227	9	AK074975	AK074975	Homo sapi
	7	216	100.0	2293	6	AX879422	AX879422	Sequence
	8	216	100.0	2293	6	BD157826	BD157826	Primer fo
	9	216	100.0	2293	9	AK027471	AK027471	Homo sapi
	10	216	100.0	2306	6	AX882662	AX882662	Sequence
	11	216	100.0	2306	6	BD159853	BD159853	Primer fo
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	15	216	100.0	3041	9	AK027501	AK027501	Homo sapi
	16	216	100.0	3093	6	AX026741	AX026741	Sequence
	17	216	100.0	3333	6	BD274939	BD274939	POLYNUCLE
	18	216	100.0	3498	6	BD274938	BD274938	POLYNUCLE
	19	216	100.0	3550	6	AX099520	AX099520	Sequence
	20	216	100.0	3550	6	BD190797	BD190797	Secreted
	21	216	100.0	3634	9	AK096337	AK096337	Homo sapi
	22	216	100.0	3862	6	AX026746	AX026746	Sequence
	23	216	100.0	3862	9	AF279656	AF279656	Homo sapi
	24	216	100.0	4250	9	AB037789	AB037789	Homo sapi
	25	216	100.0	4982	6	AX780545	AX780545	Sequence
	26	216	100.0	6060	6	AX884099	AX884099	Sequence
	27	216	100.0	6060	6	BD160721	BD160721	Primer fo
	28	216	100.0	6060	9	AK027867	AK027867	Homo sapi
	29	216	100.0	131823	2	AC010497	AC010497	Homo sapi
c	30	216	100.0	134349	9	AC010296	AC010296	Homo sapi
	31	216	100.0	154061	9	AC008524	AC008524	Homo sapi
	32	216	100.0	179647	2	AC108124	AC108124	Homo sapi
c	33	216	100.0	188207	2	AC010233	AC010233	Homo sapi

c	34	212.8	98.5	56835	2	AC025369	AC025369 Homo sapi
	35	195.2	90.4	3018	10	AF288666	AF288666 Mus muscu
	36	193.6	89.6	4139	10	BC062979	BC062979 Mus muscu
	37	193.6	89.6	4702	10	BC059238	BC059238 Mus muscu
	38	193.6	89.6	169529	10	AC124466	AC124466 Mus muscu
c	39	193.6	89.6	170386	2	AC124181	AC124181 Mus muscu
	40	193.6	89.6	184366	10	AC121783	AC121783 Mus muscu
	41	193.6	89.6	237974	2	AC094771	AC094771 Rattus no
c	42	193.6	89.6	253924	2	AC126707	AC126707 Rattus no
	43	193.6	89.6	258786	2	AC125773	AC125773 Rattus no
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ALIGNMENTS

RESULT 1

AX026743

LOCUS AX026743 216 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 3 from Patent WO0031252.

ACCESSION AX026743

VERSION AX026743.1 GI:10187888

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Klostermann,A. and Behl,C.

TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

JOURNAL Patent: WO 0031252-A 3 02-JUN-2000; KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN (DE)

FEATURES Location/Qualifiers

source

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

CDS

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/note="unnamed protein product"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e-41;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      1 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
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Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216

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RESULT 2

AX876167

LOCUS AX876167 2123 bp DNA linear PAT 17-DEC-2003

DEFINITION Sequence 11072 from Patent EP1074617.

ACCESSION AX876167

VERSION AX876167.1 GI:40030903

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesising full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 11072 07-FEB-2001; Research Association for Biotechnology (JP)

FEATURES

source Location/Qualifiers

1. .2123

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

CDS

127. .1650

/note="unnamed protein product"

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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2123;

Best Local Similarity 100.0%; Pred. No. 9.2e-42;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
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Db      1492 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 1551

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db      1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647

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RESULT 3

BD155987

LOCUS BD155987 2123 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD155987

VERSION BD155987.1 GI:27861745

KEYWORDS JP 2002191363-A/10830.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2123)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 10830 09-JUL-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/10830

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,

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Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT CDS (127)..(1647).

FEATURES Location/Qualifiers

source 1..2123

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2123;

Best Local Similarity 100.0%; Pred. No. 9.2e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TACTGACAAGGTCTG 120
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Db      1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647
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RESULT 4

AK027439

LOCUS AK027439 2123 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14533 fis, clone NT2RM2000407, moderately similar to Mus musculus semaphorin VIa mRNA.

ACCESSION AK027439

VERSION AK027439.1 GI:14042113

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2123)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES Location/Qualifiers

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ORIGIN

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Qy      61  CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
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Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
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Db      1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 1611

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db      1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647

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RESULT 5

BD127394

LOCUS BD127394 2227 bp DNA linear PAT 18-SEP-2002

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD127394

VERSION BD127394.1 GI:23222339

KEYWORDS JP 2002017375-A/2825.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2227)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002017375-A 2825 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/2825
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT CDS (56)..(1741).
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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RESULT 6

AK074975

LOCUS AK074975 2227 bp mRNA linear PRI 03-SEP-2002

DEFINITION Homo sapiens cDNA FLJ90494 fis, clone NT2RP3003614.

ACCESSION AK074975

VERSION AK074975.1 GI:22760768

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2227)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"
/clone="NT2RP3003614"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP3"
/note="cloning vector: pME18SFL3~mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
induction"

CDS 56. .1744
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ORIGIN

Query Match

100.0%; Score 216; DB 9; Length 2227;

Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCTTTGCTCCC 1705

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RESULT 7

AX879422

LOCUS AX879422 2293 bp DNA linear PAT 17-DEC-2003

DEFINITION Sequence 14327 from Patent EP1074617.

ACCESSION AX879422

VERSION AX879422.1 GI:40034158

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesising full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 14327 07-FEB-2001;

Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers

source

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/db_xref="taxon:9606"

CDS

138. .1826

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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2293;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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RESULT 8

BD157826

LOCUS BD157826 2293 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD157826

VERSION BD157826.1 GI:27863584

KEYWORDS JP 2002191363-A/12669.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2293)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 12669 09-JUL-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/12669

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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 Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT CDS (138)..(1823).

FEATURES Location/Qualifiers

source 1..2293

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/mol_type="genomic DNA"
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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2293;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db 1608 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
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Db 1668 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 1727

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db 1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1787

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|
Db 1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823

RESULT 9

AK027471

LOCUS AK027471 2293 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14565 fis, clone NT2RM4000233, highly similar to Mus musculus semaphorin VIa mRNA.

ACCESSION AK027471

VERSION AK027471.1 GI:14042170

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2293)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction,

5'- & 3'-end one pass sequencing and clone selection: Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

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FEATURES             Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2293;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 1727

Qy     121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
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Qy     181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||||||
Db     1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823
  
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RESULT 10

AX882662

LOCUS AX882662 2306 bp DNA linear PAT 17-DEC-2003
 DEFINITION Sequence 17567 from Patent EP1074617.

ACCESSION AX882662
 VERSION AX882662.1 GI:40037563
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesising full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 17567 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2306;
 Best Local Similarity 100.0%; Pred. No. 9.1e-42;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 1794
 Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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 Db 1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830

RESULT 11

BD159853

LOCUS BD159853 2306 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD159853

VERSION BD159853.1 GI:27865611

KEYWORDS JP 2002191363-A/14696.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2306)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 14696 09-JUL-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/14696

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,

PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers

FT CDS (109)..(1830).

FEATURES Location/Qualifiers

source

1..2306

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 2306;

Best Local Similarity 100.0%; Pred. No. 9.1e-42;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||

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Db 1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830

RESULT 12

AK027654

LOCUS AK027654 2306 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14748 fis, clone NT2RP3002869, highly similar to Mus musculus semaphorin VIa mRNA.

ACCESSION AK027654

VERSION AK027654.1 GI:14042491

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2306)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES Location/Qualifiers

source

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CDS

109. .1833

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MKPNDACT"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 2306;
Best Local Similarity 100.0%; Pred. No. 9.1e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||||
Db 1615 CCGCCGCCCCGCCCCGAGAGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674
Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
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Db 1675 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 1734
Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
|||||
Db 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1794
Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db 1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830

RESULT 13

AX882248

LOCUS AX882248 3041 bp DNA linear PAT 17-DEC-2003

DEFINITION Sequence 17153 from Patent EP1074617.

ACCESSION AX882248

VERSION AX882248.1 GI:40037065

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesising full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 17153 07-FEB-2001;
Research Association for Biotechnology (JP)

FEATURES Location/Qualifiers

source 1. .3041
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

CDS 85. .2184
/note="unnamed protein product"
/codon_start=1

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ERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFRLTMVRYRLTKIAVDTAAGPYQ
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LDRASSSLYVAFSTCVIKVPLGR CERH GKCKKTCIASRDPYCGWIEGGACSHLSPNS
RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLPSTTTSDSTAQEGYESRGGMLDWK
HLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDLVLPVTLIAIIVILAFVMGAVF
SGITVYCVCDHRRKDVAVVQRKEKELTHSRGSMSSVTKL SGLFGDTQSKDPKPEAIL
TPLMHNGKLATPGNTAKMLIKADQHHLDTALPTPESTPTLQQKRKPSRGSREWERNQ
NLINACTKDMPPMGSPVPTDPLRASPSHIPSVVVLPIITQQGYQHEYVDQPKMSEVA
QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQ
TGLSKRLEMHHSSSYGV DYKRSYPTNSLTRSHQATTLKRNTNTSSNSSHL SRNQSFGR
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PSFAPLSTSMKPNDACT"

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ORIGIN

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Query Match          100.0%;  Score 216;  DB 6;  Length 3041;
Best Local Similarity 100.0%;  Pred. No. 8.8e-42;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC  60
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Qy      61  CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCCTACAAC TACTGACAAGGTCG 120
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Db      2026 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCCTACAAC TACTGACAAGGTCG 2085

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181

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RESULT 14

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BD159617
LOCUS      BD159617                      3041 bp    DNA        linear    PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION  BD159617
VERSION    BD159617.1  GI:27865375
KEYWORDS   JP 2002191363-A/14460.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 3041)
  AUTHORS  Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE    Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 14460 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT    OS  Homo sapiens (human)
            PN  JP 2002191363-A/14460

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PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
PC

C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,

PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers

FT CDS (85)..(2181).

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

Query Match 100.0%; Score 216; DB 6; Length 3041;
Best Local Similarity 100.0%; Pred. No. 8.8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||||
Db 1966 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025
Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCTG 120
|||||
Db 2026 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCTG 2085
Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
|||||
Db 2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145
Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|||||
Db 2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181

RESULT 15

AK027501

LOCUS AK027501 3041 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14595 fis, clone NT2RM4002194, highly similar
to Mus musculus semaphorin VIa mRNA.

ACCESSION AK027501

VERSION AK027501.1 GI:14042222

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,

Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3041)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4002194"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RM4"
/note="cloning vector: pUC19FL3~mRNA from uninduced NT2
neuronal precursor cells."

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PSFAPLSTSMKPNDACT"

ORIGIN

Query Match 100.0%; Score 216; DB 9; Length 3041;
Best Local Similarity 100.0%; Pred. No. 8.8e-42;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||||

Db 1966 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
        |||
Db      2026 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2085

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        |||
Db      2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
        |||
Db      2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181

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Job time : 859.974 secs

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 19:45:25 ; Search time 86.4914 Seconds
 (without alignments)
 10609.274 Million cell updates/sec

Title: US-09-856-681A-3
 Perfect score: 216
 Sequence: 1 ccgccgcccccccgagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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3	216	100.0	2123	4	AAH13995	Aah13995 Human cDN
4	216	100.0	2227	4	AAK94365	Aak94365 Human ful
5	216	100.0	2262	6	ABK34739	Abk34739 Human cDN
6	216	100.0	2293	4	AAH15834	Aah15834 Human cDN
7	216	100.0	2306	4	AAH17861	Aah17861 Human cDN

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	9	216	100.0	3039	5	AAS68807	Aas68807	DNA	encod
	10	216	100.0	3039	5	AAS89721	Aas89721	DNA	encod
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	12	216	100.0	3333	3	AAA93618	Aaa93618	Human	sem
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	14	216	100.0	3498	3	AAA93617	Aaa93617	Human	sem
	15	216	100.0	3498	8	ADA23280	Ada23280	cDNA	enco
	16	216	100.0	3550	2	AAV44295	Aav44295	Human	sec
	17	216	100.0	3550	5	AAF98469	Aaf98469	Human	cDN
	18	216	100.0	3862	3	AAD01233	Aad01233	Human	sem
	19	216	100.0	4250	8	ADA23361	Ada23361	cDNA	enco
	20	216	100.0	4280	7	ABX71103	Abx71103	Novel	hum
	21	216	100.0	4564	8	ACH03994	Ach03994	Human	cDN
	22	216	100.0	6060	4	AAH18729	Aah18729	Human	cDN
c	23	168	77.8	460	8	ACH16587	Ach16587	Human	adu
	24	55	25.5	1853	4	AAH15994	Aah15994	Human	cDN
	25	55	25.5	2581	4	AAH16063	Aah16063	Human	cDN
	26	55	25.5	3196	6	ABS64382	Abs64382	Human	sem
	27	55	25.5	3205	6	ABS64380	Abs64380	Human	sem
	28	55	25.5	3364	6	ABS64384	Abs64384	Human	sem
	29	55	25.5	3694	4	AAH42597	Aah42597	Nucleotid	
	30	55	25.5	4234	6	ABA00055	Aba00055	CADHP-2	c
	31	55	25.5	6645	7	ABX34714	Abx34714	Human	mdd
	32	55	25.5	6767	4	AAL04256	Aal04256	Human	rep
	33	55	25.5	6773	4	AAL04255	Aal04255	Human	rep
	34	53.4	24.7	662	4	AAL00809	Aal00809	Human	rep
c	35	42.8	19.8	575	4	AAH10827	Aah10827	Human	cDN
	36	36.8	17.0	670	5	AAC90703	Aac90703	Human	sec
c	37	35.4	16.4	1971	2	AAV58278	Aav58278	Fluoresce	
	38	35.2	16.3	936	7	ABT21228	Abt21228	Aspergill	
	39	35.2	16.3	936	7	ABT19408	Abt19408	Aspergill	
	40	35.2	16.3	1015	7	ABT18814	Abt18814	Aspergill	
	41	35.2	16.3	1015	7	ABT20630	Abt20630	Aspergill	
	42	35.2	16.3	3015	7	ABT18220	Abt18220	Aspergill	
	43	35.2	16.3	3015	7	ABT20034	Abt20034	Aspergill	
c	44	35.2	16.3	13987	2	AAT80415	Aat80415	Hybrid	sr
c	45	35.2	16.3	43280	2	AAT80413	Aat80413	Tylactone	

ALIGNMENTS

RESULT 1

AAD01234

ID AAD01234 standard; DNA; 216 BP.

XX

AC AAD01234;

XX

DT 04-OCT-2000 (first entry)

XX

DE DNA encoding binding domain of human semaphorin 6A-1.

XX

KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;

KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;

KW gene therapy; diagnostic agent; therapeutic agent; differentiation;

KW cytoskeletal stabilisation; plasticity; ds.

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OS   Homo sapiens.
XX
FH   Key                Location/Qualifiers
FT   CDS                1. .216
FT                        /*tag= a
FT                        /product= "Binding domain of semaphorin 6A-1"
FT                        /note= "The binding domain shows homology to Zyxin
FT                        protein and selectively binds to members of Ena/VASP
FT                        protein family, especially Evl; the CDS does not include
FT                        stop codon"
FT                        /partial
XX
PN   WO200031252-A1.
XX
PD   02-JUN-2000.
XX
PF   26-NOV-1999;      99WO-EP009215.
XX
PR   26-NOV-1998;      98EP-00122441.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Behl C,  Klostermann A;
XX
DR   WPI; 2000-400065/34.
DR   P-PSDB; AAY71461.
XX
PT   Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT   therapeutic agent, for modulating immune system, in gene therapy or for
PT   effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS   Claim 2; Page 21; 53pp; English.
XX
CC   The present sequence is a DNA encoding binding domain of transmembranous
CC   human semaphorin 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal
CC   development and regeneration mechanisms during apoptosis. The binding
CC   domain shows homology to Zyxin protein and selectively binds to members
CC   of Ena/VASP protein family, especially Evl. (HSA)SEMA6A-1 is a member of
CC   protein family displaying secreted or transmembrane-based repulsive
CC   guidance cues critically involved in neuronal development. Expression of
CC   (HSA)SEMA6A-1 is highest in embryonic brain and kidney and moderate in
CC   lung. The present sequence is useful as diagnostic and therapeutic
CC   agents, for modulating the immune system, in gene therapy, for effecting
CC   differentiation, cytoskeletal stabilisation and plasticity
XX
SQ   Sequence 216 BP; 45 A; 85 C; 51 G; 35 T; 0 U; 0 Other;

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Query Match          100.0%;  Score 216;  DB 3;  Length 216;
Best Local Similarity 100.0%;  Pred. No. 2.7e-52;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||||||||
Db      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216

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RESULT 2

AAC98050

ID AAC98050 standard; cDNA; 1472 BP.

XX

AC AAC98050;

XX

DT 09-MAR-2001 (first entry)

XX

DE Human colon cancer antigen nucleotide sequence SEQ ID NO:60.

XX

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200055351-A1.

XX

PD 21-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-US005883.

XX

PR 12-MAR-1999; 99US-0124270P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2000-587534/55.

DR

P-PSDB; AAB53293.

XX

PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.

XX

PS Claim 1; Page 510-511; 2104pp; English.

XX

CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,

CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
 CC sequences used in the exemplification of the present invention

XX

SQ Sequence 1472 BP; 437 A; 431 C; 299 G; 301 T; 0 U; 4 Other;

Query Match 100.0%; Score 216; DB 3; Length 1472;
 Best Local Similarity 100.0%; Pred. No. 4.3e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
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Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
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 Db 492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 551

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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 Db 552 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 587

RESULT 3

AAH13995

ID AAH13995 standard; cDNA; 2123 BP.

XX

AC AAH13995;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:11072.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.

XX

PS Claim 8; SEQ ID NO 11072; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 2123 BP; 550 A; 664 C; 528 G; 381 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2123;
Best Local Similarity 100.0%; Pred. No. 4.7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|
Db 1432 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1491

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
|
Db 1492 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 1551

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
|

Db 1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
 |||

Db 1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647

RESULT 4

AAK94365

ID AAK94365 standard; cDNA; 2227 BP.

XX

AC AAK94365;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human full-length cDNA, SEQ ID NO: 3087.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-00114089.

XX

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI; 2001-524255/58.

DR P-PSDB; AAM93444.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.

XX

PS Claim 8; SEQ ID NO 3087; 1380pp + Sequence Listing; English.

XX

CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesising the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a full length human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in CD-ROM format directly
 CC from EPO

XX

SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2227;
Best Local Similarity 100.0%; Pred. No. 4.7e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      1526 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1585

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCG 120
          |||
Db      1586 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCG 1645

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1705

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      1706 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1741
```

RESULT 5

ABK34739

ID ABK34739 standard; cDNA; 2262 BP.

XX

AC ABK34739;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human cDNA for novel secreted protein, SEQ ID 508.

XX

KW Human; ss; gene; secreted protein; immune deficiency; viral infection;
KW bacterial infection; fungal infection; autoimmune disorder; burn;
KW rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW lymphoid cell deficiency.

XX

OS Homo sapiens.

XX

PN WO200177290-A2.

XX

PD 18-OCT-2001.

XX

PF 29-MAR-2001; 2001WO-US010295.

XX

PR 06-APR-2000; 2000US-0194941P.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;

PI Gulukota K, Graham JR;

XX

DR WPI; 2002-179323/23.
 XX
 PT Six hundred and twenty five polynucleotides derived from a variety of
 PT human tissue sources which encode secreted proteins, useful for treating
 PT immune deficiencies and disorders such as autoimmune disorders.
 XX
 PS Claim 1; Page 272; 339pp; English.
 XX
 CC The invention relates to 625 polynucleotides which have been derived from
 CC a variety of human tissue sources and which encode novel secreted
 CC proteins, their complements and sequences that hybridise to them. Also
 CC included are a vector comprising the polynucleotide, a host cell
 CC transformed with the vector, the proteins encoded by the polynucleotides,
 CC antibodies that bind to the proteins and identification of modulators of
 CC the proteins or the expression of the polynucleotide. The polynucleotides
 CC can be used as probes for the identification and isolation of full length
 CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
 CC as nutritional supplements. The protein is useful in the treatment of
 CC various immune deficiencies and disorders such as viral infections,
 CC bacterial infections, fungal infections, autoimmune disorders (e.g.
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
 CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
 CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
 CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
 CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
 CC tumours. They are also useful for tissue regeneration, for wound healing
 CC and in the treatment of burns, incisions and ulcers. The proteins are
 CC also useful for regulating haematopoiesis, for treating myeloid or
 CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
 CC sequences encoding a secreted protein
 XX
 SQ Sequence 2262 BP; 604 A; 695 C; 522 G; 441 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 6; Length 2262;
 Best Local Similarity 100.0%; Pred. No. 4.7e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1184 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1243
 Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1244 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 1303
 Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1304 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 1363
 Qy 181 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 216
 ||||||||||||||||||||||||||||||||||||
 Db 1364 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 1399

RESULT 6
 AAH15834
 ID AAH15834 standard; cDNA; 2293 BP.

XX
 AC AAH15834;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:14327.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 14327; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC oligonucleotides, all of which are used in the exemplification of the
CC present invention

XX

SQ Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2293;
Best Local Similarity 100.0%; Pred. No. 4.8e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      1608 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          |||
Db      1668 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 1727

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1787

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823
```

RESULT 7

AAH17861

ID AAH17861 standard; cDNA; 2306 BP.

XX

AC AAH17861;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:17567.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 XX
 PS Claim 8; SEQ ID NO 17567; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 4; Length 2306;
 Best Local Similarity 100.0%; Pred. No. 4.8e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1615 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674
 Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1675 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 1734
 Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1794
 Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
 ||||||||||||||||||||||||||||||||||||
 Db 1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830

RESULT 8
 AAS68253

ID AAS68253 standard; cDNA; 2592 BP.
 XX
 AC AAS68253;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #4057.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG04066.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 4057; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

QX Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 5; Length 2592;

Best Local Similarity 100.0%; Pred. No. 4.9e-52;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

|||||

Db 2374 CCGCCGCCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2433

QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120

|||||

Db 2434 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2493

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180

|||||

Db 2494 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2553

QY 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216

|||||

Db 2554 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2589

RESULT 9

AAS68807

ID AAS68807 standard; cDNA; 3039 BP.

XX

AC AAS68807;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #4611.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG04620.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 5; Length 3039;
Best Local Similarity 100.0%; Pred. No. 5.1e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCGCCGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	60
Db	2821	CCGCCGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC	2880
Qy	61	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCTG	120
Db	2881	CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCTG	2940
Qy	121	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC	180
Db	2941	GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC	3000
Qy	181	CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA	216
Db	3001	CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA	3036

RESULT 10

XX
 DE DNA encoding novel human diagnostic protein #25525.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG25534.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 25525; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 100.0%; Score 216; DB 5; Length 3039;
 Best Local Similarity 100.0%; Pred. No. 5.1e-52;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      2821 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2880

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          |||
Db      2881 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2940

Qy     121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db     2941 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3000

Qy     181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db     3001 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3036

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RESULT 11

AAH17625

ID AAH17625 standard; cDNA; 3041 BP.

XX

AC AAH17625;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:17153.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US006280.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 08-MAR-2000; 2000US-0520781P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;
 XX
 DR WPI; 2000-594318/56.
 DR P-PSDB; AAB23031.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders.
 XX
 PS Claim 3; Fig 3; 151pp; English.
 XX
 CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
 CC the invention are either secreted or membrane-associated proteins and act
 CC as regulator of cellular proliferation and differentiation. SECX proteins
 CC or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of a
 CC SECX protein with other cellular proteins may be useful to modulate the
 CC activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in a
 CC biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders

CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 3; Length 3333;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db 2925 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
|
Db 2985 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 3044

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
|
Db 3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 3104

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
|
Db 3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140

RESULT 13

ADA23282

ID ADA23282 standard; cDNA; 3333 BP.

XX

AC ADA23282;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC3 #1.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;

KW antiallergic; cardiant; dermatological; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

XX

PR 04-JAN-2000: 2000US-0174485P.

PR 19-SEP-2000; 2000US-0233798P.

XX

PA (LARO/) LAROCHELLE W J.

PI Shimkets RA, Larochelle WJ;

DB WPT: 2003-540616/51.

XX

PT e.g., lung cancer, cardiovasc

XX and dactylinane disease.

15 claim 3, fig 3, 110pp, English
 22

membrane-associated (SECY) po

screening for a modulator of

CC preventing SECY-associated di-

CC rejection allergy AIDS inf

neurological diseases (e.g. Alzheimer's disease).

CC SECY polypeptide of the inver

Sequence 3333 BP. 874 A. 921

Query Match 100.0%

Best Local Similarity 100.0%,
Matches 316: Conservative 6

C:: 1 GGGGGGGGGGGGGGGGGGGGACAC

Pt	2025	GGGGGGGGGGGGGGGGGGGAGAG

0 61 GGGGGGCTGAGTCTCTCTGCGAG

D1 0005 | | | | | | | | | | | | | | | | | |

 0005 G A C G G G C G T C G C T G T G T G C G C

0 101 000000011000000000000000

Query Match 100.0%; Score 216; DB 8; Length 3333;

Best Local Similarity 100.0%; Pred. No. 5.2e-52;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

Db 2925 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

QY 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TCACTGACAAGGTCG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 3044

QY 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180

Db 3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3104

Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
 |||||

Db 3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140

RESULT 14

AAA93617

ID AAA93617 standard; DNA; 3498 BP.

XX

AC AAA93617;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.

XX

OS Homo sapiens.

XX

PN WO200053742-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR P-PSDB; AAB23030.

XX

PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 3; Fig 2; 151pp; English.

XX

CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular

CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in a
 CC biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 3; Length 3498;
 Best Local Similarity 100.0%; Pred. No. 5.3e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3090 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149

Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3150 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 3209

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3269

Qy 181 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 216
 ||||||||||||||||||||||||||||||||||||
 Db 3270 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 3305

RESULT 15

ADA23280

ID ADA23280 standard; cDNA; 3498 BP.

XX

AC ADA23280;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
 KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
 KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
 KW cardiovascular disease; oncology disease; immune disorder;
 KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
 KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
 KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
 KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
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PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochele WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23281.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Fig 2; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 100.0%; Score 216; DB 8; Length 3498;
Best Local Similarity 100.0%; Pred. No. 5.3e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCCGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|||||
Db 3090 CCGCCGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149
Qy 61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
|||||

```

Db      3150 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAAC TCACTGACAAGGTCG 3209
Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3269
Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
        |||||||||||||||||||||||||||||||||||
Db      3270 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3305

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Search completed: March 26, 2004, 00:01:21
 Job time : 87.4914 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:24:56 ; Search time 15.7969 Seconds
(without alignments)
7588.151 Million cell updates/sec

Title: US-09-856-681A-3
Perfect score: 216
Sequence: 1 cgcgcgccccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		8					Description
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	1	55	25.5	3261	4	US-09-653-274-5	Sequence 5, Appli
	2	55	25.5	3694	4	US-09-653-274-3	Sequence 3, Appli
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c	4	35.4	16.4	1971	3	US-08-818-252-7	Sequence 7, Appli
c	5	35.2	16.3	13987	2	US-08-804-227C-13	Sequence 13, Appl
c	6	35.2	16.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
c	7	34.4	15.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	8	34.4	15.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	9	33.8	15.6	846	4	US-09-252-991A-8905	Sequence 8905, Ap
	10	33.8	15.6	1026	4	US-09-252-991A-1737	Sequence 1737, Ap
	11	33.8	15.6	2667	4	US-09-252-991A-9254	Sequence 9254, Ap

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c	14	33.2	15.4	630	4	US-09-252-991A-7012	Sequence 7012, Ap
	15	33.2	15.4	1548	4	US-09-252-991A-7061	Sequence 7061, Ap
	16	33.2	15.4	1581	4	US-09-252-991A-7117	Sequence 7117, Ap
	17	33	15.3	1536	3	US-08-993-359-29	Sequence 29, Appl
	18	33	15.3	1536	4	US-09-482-558A-29	Sequence 29, Appl
	19	32	14.8	1153	2	US-08-869-793-5	Sequence 5, Appli
	20	32	14.8	1162	4	US-09-620-312D-982	Sequence 982, App
	21	31.8	14.7	1119	4	US-09-170-496D-65	Sequence 65, Appl
	22	31.8	14.7	1119	4	US-09-170-496D-199	Sequence 199, App
	23	31.8	14.7	1679	1	US-08-202-056-6	Sequence 6, Appli
	24	31.8	14.7	1679	1	US-08-076-093A-5	Sequence 5, Appli
	25	31.8	14.7	1679	1	US-08-701-265-5	Sequence 5, Appli
	26	31.8	14.7	1679	2	US-08-284-586-5	Sequence 5, Appli
	27	31.8	14.7	1679	2	US-08-805-478-5	Sequence 5, Appli
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	31	31.8	14.7	1679	3	US-09-104-296-5	Sequence 5, Appli
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	37	31.2	14.4	1320	3	US-09-221-654-1	Sequence 1, Appli
	38	31.2	14.4	1320	3	US-08-989-358A-1	Sequence 1, Appli
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c	45	30.4	14.1	77536	4	US-09-410-551B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-653-274-5

; Sequence 5, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-653-274-5

Query Match 25.5%; Score 55; DB 4; Length 3261;
Best Local Similarity 64.6%; Pred. No. 8.1e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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Db      3113 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGA 3172

Qy      134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCA 193
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Qy      194 TGAAGCC 200
      | | ||
Db      3233 TCAGACC 3239
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RESULT 2

US-09-653-274-3

; Sequence 3, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (434)..(3694)
US-09-653-274-3

Query Match 25.5%; Score 55; DB 4; Length 3694;

Best Local Similarity 64.6%; Pred. No. 8.3e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```
Qy      74 TCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTA 133
      ||| || ||| ||| || | | | | | ||| ||| ||| |||
Db      3546 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGA 3605

Qy      134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCA 193
      ||| || ||| || |||| || || || || |||| ||| | || |||
Db      3606 CGCCGTCCTTAAACCTGACGTGCCACCAAAGCCTTCCTTTGTTTCCTCAAACCCCATCTG 3665

Qy      194 TGAAGCC 200
      | | ||
Db      3666 TCAGACC 3672
```

RESULT 3

US-08-818-253-7/c

```
; Sequence 7, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1971 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1968
US-08-818-253-7

Query Match 16.4%; Score 35.4; DB 2; Length 1971;
Best Local Similarity 61.3%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
Qy      2 CGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
        ||||| || | || ||| ||| | ||| || ||||| ||||| ||| | |
Db     112 CGCCGTCCAGCTCGACCAGGATGGGCACCAACCCCGGTGAACAGCTCCTCGCCCTTGCTCA 53

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
        ||| ||| | || ||||| ||
Db     52 CGTCGGCGGCGGCCGCCCAGCAGGCCAGCAGCA 20
```

RESULT 4
US-08-818-252-7/c
; Sequence 7, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/818,252B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (0)...(1968)
US-08-818-252-7

Query Match 16.4%; Score 35.4; DB 3; Length 1971;
Best Local Similarity 61.3%; Pred. No. 0.34;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
Qy      2 CGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
        ||||| || | || ||| ||| | ||| || ||||| ||||| ||| | |
Db     112 CGCCGTCCAGCTCGACCAGGATGGGCACCAACCCCGGTGAACAGCTCCTCGCCCTTGCTCA 53

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
        ||| ||| | || ||||| ||
Db     52 CGTCGGCGGCGGCCGCCCAGCAGGCCAGCAGCA 20
```

RESULT 5
US-08-804-227C-13/c


```

; Sequence 13, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
;   APPLICANT: DeHoff, Bradley S.
;   APPLICANT: Kuhstoss, Stuart A.
;   APPLICANT: Rosteck, Paul R., Jr.
;   APPLICANT: Sutton, Kimberly L.
;   TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: THOMAS G. PLANT 1501
;     STREET: LILLY CORPORATE CENTER
;     CITY: INDIANAPOLIS
;     STATE: IN
;     COUNTRY: USA
;     ZIP: 46285
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: ASCI(DOS) Text only
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/804,227C
;     FILING DATE: February 21, 1997
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Plant, Thomas, G.
;     REGISTRATION NUMBER: 35,784
;     REFERENCE/DOCKET NUMBER: X-8231
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 317-276-2459
;   INFORMATION FOR SEQ ID NO: 13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 13987 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 350..13987
US-08-804-227C-13

```

```

Query Match          16.3%; Score 35.2; DB 2; Length 13987;
Best Local Similarity 48.5%; Pred. No. 0.67;
Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

```

```

Qy      2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
      || || || | || | || | || | || | || | || | ||
Db      1346 CGGCGAGCGGCGTGCTGCGGCCGCTGTCCGCCCCGCCCCGAGCACGGCGCCAGTGCGG 1287

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGG 121
      ||| ||| | ||| | | | | | | | | | | | | | |
Db      1286 CCGCTCGACGGGGTCGCCGGCCCCGGGTGCCGGTCCCGTGCAGCTCGACGTAGCGGACGG 1227

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
      || | || ||||| | | | | | | | | | | | | | |

```

Db 1226 CGCCGGTGCTGACGCCCCGCCCGGTTAGGCCTGGCGCAGCACAGCTTCCTGCGCCTCCC 1167

Qy 182 TTTCCACATCCATGAAGCCC 201

|| | ||| |||

Db 1166 GGTCGGGAGTGGTGAGGCTC 1147

RESULT 6

US-08-804-227C-1/c

; Sequence 1, Application US/08804227C

; Patent No. 5876991

; GENERAL INFORMATION:

; APPLICANT: DeHoff, Bradley S.

; APPLICANT: Kuhstoss, Stuart A.

; APPLICANT: Rosteck, Paul R., Jr.

; APPLICANT: Sutton, Kimberly L.

; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: THOMAS G. PLANT 1501

; STREET: LILLY CORPORATE CENTER

; CITY: INDIANAPOLIS

; STATE: IN

; COUNTRY: USA

; ZIP: 46285

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCI(DOS) Text only

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/804,227C

; FILING DATE: February 21, 1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Plant, Thomas, G.

; REGISTRATION NUMBER: 35,784

; REFERENCE/DOCKET NUMBER: X-8231

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317-276-2459

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43280 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 816..14234

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 14351..19945

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20010..31199

; FEATURE:

```

; NAME/KEY: CDS
; LOCATION: 31232..36067
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36249..41774
US-08-804-227C-1

```

```

Query Match          16.3%; Score 35.2; DB 2; Length 43280;
Best Local Similarity 48.5%; Pred. No. 0.91;
Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

```

```

Qy      2 CGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
      || || || | || | || | || | || | || | || | ||
Db      1896 CGGCGAGCGGCGTGTGCGGCCGCTGTCCGCCCCCGCCCCGAGCACGGCGCCAGTGCGG 1837

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGG 121
      ||| ||| | ||| | | | | | | | | | | | | | |
Db      1836 CCGCCTCGACGGGGTGC CGCGGCCCGGGTGC CGGTCCCGTGCAGCTCGACGTAGCGGACGG 1777

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCC 181
      || | || ||||| | | | | | | | | | | | | | |
Db      1776 CGCCGGTGCTGACGCCCCGCCCGCGGTAGGCCTGGCGCAGCACAGCTTCTTGCCTCCC 1717

Qy      182 TTTCCACATCCATGAAGCCC 201
      || | ||| || |
Db      1716 GGTCGGGAGTGGTGAGGCTC 1697

```

RESULT 7

US-09-103-840A-2/c

```

; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g

```

US-09-103-840A-2

```

Query Match          15.9%; Score 34.4; DB 3; Length 4403765;
Best Local Similarity 57.4%; Pred. No. 5.3;
Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

```

Qy 22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
 | | | | | | | | | | | | | | | | | | | | | |
 Db 745995 GGGTATTCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGGCGATCAGCTGGCGG
 745936

Qy 82 CAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAG 129
 | | | | | | | | | | | | | | | | | | | | | |
 Db 745935 CCGTCCTGCACCAGCGACGACAACGCCCCGCCACGCTCGGGGTCGACG 745888

RESULT 8
 US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 15.9%; Score 34.4; DB 3; Length 4411529;
 Best Local Similarity 57.4%; Pred. No. 5.3;
 Matches 62; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
 | | | | | | | | | | | | | | | | | | | | | |
 Db 744035 GGGTATTCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGGCGATCAGCTGGCGG
 743976

Qy 82 CAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAG 129
 | | | | | | | | | | | | | | | | | | | | | |
 Db 743975 CCGTCCTGCACCAGCGACGACAACGCCCCGCCACGCTCGGGGTCGACG 743928

RESULT 9
 US-09-252-991A-8905/c
 ; Sequence 8905, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8905
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8905
```

```
Query Match          15.6%; Score 33.8; DB 4; Length 846;
Best Local Similarity 49.2%; Pred. No. 0.79;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
```

```
Qy      2 CGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
      || || | ||| | | ||||| ||| || || | | |||
Db      343 CGTGGCAGCGCGAGCACATCTTCTGCGCCATCGCCTTGCCGCGCGCCAGGTCGGCGGGCG 284

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGG 121
      | ||| | | | | | ||| || | || | | |||
Db      283 CGTCCGGGCGCGGCACGGCGGGCGGCCAGCGGCAGGGAAAGCAGGGCCGAGAGGCAGCCGG 224

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
      |||| | ||| | | || | |||| | ||| || | | |
Db      223 CCAGCCAGCGTTTACGCTCAGTCATGCTGCCAGGGCCCCCGCAGCCAGCCGTGGATGTCG 164

Qy      182 T 182
      |
Db      163 T 163
```

RESULT 10

```
US-09-252-991A-1737
; Sequence 1737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1737
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1737
```

Query Match 15.6%; Score 33.8; DB 4; Length 1026;
Best Local Similarity 54.4%; Pred. No. 0.84;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```
Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGG 121
      ||||| | || || || || | || || | || || | |||||
Db      271 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 330

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
      | |||| | || | | |||| | |||| | || || | ||
Db      331 GAAGGAAGAGCGCGGCAACAAGGGCGCCCGCTGACCACCTTCATCAGCCTGGCCGGCCG 390

Qy      182 TTTCC 186
      || ||
Db      391 TTACC 395
```

RESULT 11

US-09-252-991A-9254
; Sequence 9254, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9254
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9254

Query Match 15.6%; Score 33.8; DB 4; Length 2667;
Best Local Similarity 49.2%; Pred. No. 1.1;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

```
Qy      2 CGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
      || || | ||| | | |||| || | || | |||
Db      38 CGTGGCAGCGCGAGCACATCTTCTGCGCCATCGCCTTGCCGCGCGCCAGGTCCGGCGGGCG 97

Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGG 121
      | ||| | || | || | |||| || | || | |||
Db      98 CGTCCGGGCCCCGCACGGCGGCGGCCAGCGGCAGGGAAGCAGGGCCGAGAGGCAGCCGG 157

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
      |||| | || | || | |||| | || || | || |
Db      158 CCAGCCAGCGTTTACGCTCAGTCATGCTGCCAGGGCCCCCGCAGCCAGCCGTGGATGTCTG 217
```

Qy	182	T	182
Db	218	T	218

RESULT 12

US-09-252-991A-1816

; Sequence 1816, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

: APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

; FILE REFERENCE: 107196.136

```

: CURRENT APPLICATION NUMBER: US/09/252,991A

: CURRENT FILING DATE: 1999-02-18

: PRIOR APPLICATION NUMBER: US 60/074,788

: PRIOR FILING DATE: 1998-02-18

: PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEO ID NOS: 33142

; SEO ID NO 1816

```

:      LENGTH: 3228

```

; TYPE: DNA

```

: ORGANISM: Pseudomonas aeruginosa

```

US-09-252-991A-1816

Query Match 15.6%; Score 33.8; DB 4; Length 3228;

Best Local Similarity 54.4%; Pred. No. 1.1;

Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAAC TCACTGACAAGGTCGG 121

Db 303 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 362

Qy 122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCC 181

Db 363 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 422

Qy 182 TTTCC 186

Db 423 TTACC 427

RESULT 13

US-09-252-991A-2143/c

; Sequence 2143, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

: FILE REFERENCE: 107196.136

: CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2143
; LENGTH: 3546
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2143

Query Match 15.6%; Score 33.8; DB 4; Length 3546;
Best Local Similarity 54.4%; Pred. No. 1.2;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```
Qy      62 AGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGG 121
      ||||| | || ||| || || | || ||| || ||| | |||||
Db      3064 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 3005

Qy      122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
      | |||| | || | | |||| | ||| || | || ||| | ||
Db      3004 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 2945

Qy      182 TTTCC 186
      || ||
Db      2944 TTACC 2940
```

RESULT 14

US-09-252-991A-7012/c
; Sequence 7012, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7012
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7012

Query Match 15.4%; Score 33.2; DB 4; Length 630;
Best Local Similarity 53.0%; Pred. No. 1.1;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

```
Qy      7 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
      || ||| |||| | | | | | | | ||| ||| ||||| |||
```



```

Db      203 CCTGCCGCGCATCGAGGTGGATGCGGCGATCGCCGCCCGTCCCGGCCGGCTGGCCTGGCG 144
Qy      67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG 126
          | ||| | |||| | | | | | | | | |||| | |
Db      143 CATCTATCGTGGAGCCC GCCCATGAGCATGGCTTCCAGCCCGTCCCAAGGAGGCGCGAC 84
Qy      127 AAGCGTACGCCCTC 140
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Db      83 AGGCAGTCGCCCTC 70

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RESULT 15

US-09-252-991A-7061

; Sequence 7061, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 7061

; LENGTH: 1548

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-7061

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Query Match          15.4%; Score 33.2; DB 4; Length 1548;
Best Local Similarity 53.0%; Pred. No. 1.4;
Matches 71; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Qy      7 CCCGCCCCGCGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
          || ||| |||| | | | | | | | | ||| ||| ||||| |||
Db      532 CCTGCCGCGCATCGAGGTGGATGCGGCGATCGCCGCCCGTCCCGGCCGGCTGGCCTGGCG 591
Qy      67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG 126
          | ||| | |||| | | | | | | | | |||| | |
Db      592 CATCTATCGTGGAGCCC GCCCATGAGCATGGCTTCCAGCCCGTCCCAAGGAGGCGCGAC 651
Qy      127 AAGCGTACGCCCTC 140
          | || | |||||
Db      652 AGGCAGTCGCCCTC 665

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Search completed: March 26, 2004, 03:46:11

Job time : 23.7969 secs

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:27:11 ; Search time 76.6346 Seconds
(without alignments)
10493.560 Million cell updates/sec

Title: US-09-856-681A-3
Perfect score: 216
Sequence: 1 ccgccgccccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

c	1	216	100.0	569	14	US-10-029-386-11004	Sequence 11004, A
c	2	216	100.0	1199	14	US-10-029-386-24706	Sequence 24706, A
	3	216	100.0	1472	9	US-09-925-299-60	Sequence 60, Appl
	4	216	100.0	1472	10	US-09-925-299-60	Sequence 60, Appl
	5	216	100.0	2944	12	US-10-403-676-29	Sequence 29, Appl
	6	216	100.0	2944	15	US-10-449-548-29	Sequence 29, Appl
	7	216	100.0	2995	12	US-10-403-676-19	Sequence 19, Appl
	8	216	100.0	2995	15	US-10-449-548-19	Sequence 19, Appl
	9	216	100.0	3055	12	US-10-403-676-27	Sequence 27, Appl
	10	216	100.0	3055	15	US-10-449-548-27	Sequence 27, Appl
	11	216	100.0	3106	12	US-10-403-676-17	Sequence 17, Appl
	12	216	100.0	3106	15	US-10-449-548-17	Sequence 17, Appl
	13	216	100.0	3165	12	US-10-403-676-47	Sequence 47, Appl
	14	216	100.0	3165	15	US-10-449-548-47	Sequence 47, Appl
	15	216	100.0	3333	10	US-09-991-053-5	Sequence 5, Appli
	16	216	100.0	3333	10	US-09-957-187-5	Sequence 5, Appli
	17	216	100.0	3498	10	US-09-991-053-3	Sequence 3, Appli
	18	216	100.0	3498	10	US-09-957-187-3	Sequence 3, Appli
	19	216	100.0	3498	12	US-10-403-676-31	Sequence 31, Appl
	20	216	100.0	3498	15	US-10-449-548-31	Sequence 31, Appl
	21	216	100.0	3983	12	US-10-403-676-45	Sequence 45, Appl
	22	216	100.0	3983	15	US-10-449-548-45	Sequence 45, Appl
	23	216	100.0	4250	10	US-09-957-187-84	Sequence 84, Appl
	24	216	100.0	4250	12	US-10-403-676-13	Sequence 13, Appl
	25	216	100.0	4250	14	US-10-393-892-30	Sequence 30, Appl
	26	216	100.0	4250	14	US-10-394-382-30	Sequence 30, Appl
	27	216	100.0	4250	15	US-10-449-548-13	Sequence 13, Appl
	28	216	100.0	4280	15	US-10-120-988-330	Sequence 330, App
c	29	168	77.8	460	10	US-09-918-995-3799	Sequence 3799, Ap
	30	55	25.5	3196	12	US-10-016-248-15	Sequence 15, Appl
	31	55	25.5	3205	12	US-10-016-248-11	Sequence 11, Appl
	32	55	25.5	3364	12	US-10-016-248-19	Sequence 19, Appl
	33	55	25.5	6767	10	US-09-764-891-6944	Sequence 6944, Ap
	34	55	25.5	6773	10	US-09-764-891-6943	Sequence 6943, Ap
	35	53.4	24.7	662	10	US-09-764-891-810	Sequence 810, App
c	36	37.4	17.3	765	15	US-10-027-632-166826	Sequence 166826,
c	37	35.4	16.4	1971	9	US-09-554-000-7	Sequence 7, Appli
	38	35.2	16.3	936	14	US-10-128-714-2578	Sequence 2578, Ap
	39	35.2	16.3	936	14	US-10-128-714-7578	Sequence 7578, Ap
	40	35.2	16.3	1015	14	US-10-128-714-1578	Sequence 1578, Ap
	41	35.2	16.3	1015	14	US-10-128-714-6578	Sequence 6578, Ap
	42	35.2	16.3	3015	14	US-10-128-714-578	Sequence 578, App
	43	35.2	16.3	3015	14	US-10-128-714-5578	Sequence 5578, Ap
	44	35	16.2	1473	15	US-10-369-493-41703	Sequence 41703, A
c	45	34.4	15.9	31263	12	US-10-282-122A-25447	Sequence 25447, A

ALIGNMENTS

RESULT 1

US-10-029-386-11004/c

; Sequence 11004, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

```

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11004
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008524.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: gi14728537, EVALUE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: BE898612.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q62523, EVALUE 1.20e-01
US-10-029-386-11004

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Query Match          100.0%; Score 216; DB 14; Length 569;
Best Local Similarity 100.0%; Pred. No. 6.7e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      552 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 493

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      492 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCG 433

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      432 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 373

Qy      181 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 216
        ||||||||||||||||||||||||||||||||||||
Db      372 CTTTCCACATCCATGAAGCCCCAATGATGCGTGTACA 337

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RESULT 2

US-10-029-386-24706/c

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; Sequence 24706, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386

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; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24706
; LENGTH: 1199
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008524.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: gil4728537, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O35464, EVALUE 1.00e-125
; OTHER INFORMATION: EST_HUMAN HIT: AW954605.1, EVALUE 0.00e+00
US-10-029-386-24706

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Query Match          100.0%; Score 216; DB 14; Length 1199;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
        |||
Db      219 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 160

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
        |||
Db      159 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 100

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        |||
Db      99 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 40

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGGTGTACA 216
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Db      39 CTTTCCACATCCATGAAGCCCAATGATGCGGTGTACA 4

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RESULT 3

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US-09-925-299-60
; Sequence 60, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60
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```
Query Match          100.0%; Score 216; DB 9; Length 1472;
Best Local Similarity 100.0%; Pred. No. 7.4e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      372 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          |||
Db      432 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 491

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 551

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      552 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 587
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RESULT 4

US-09-925-299-60

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; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
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US-09-925-299-60

Query Match 100.0%; Score 216; DB 10; Length 1472;
Best Local Similarity 100.0%; Pred. No. 7.4e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db     372 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy     61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          |||
Db     432 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 491

Qy    121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db     492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 551

Qy    181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db     552 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 587
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RESULT 5

US-10-403-676-29

; Sequence 29, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

```

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
; LENGTH: 2944
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2944)
US-10-403-676-29

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Query Match          100.0%;  Score 216;  DB 12;  Length 2944;
Best Local Similarity 100.0%;  Pred. No. 7.9e-58;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2780 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2839

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2840 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2899

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
        ||||||||||||||||||||||||||||||||||||||||
Db      2900 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2935

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RESULT 6

US-10-449-548-29

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; Sequence 29, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochele, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
; LENGTH: 2944
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2944)
US-10-449-548-29
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Query Match          100.0%;  Score 216;  DB 15;  Length 2944;
Best Local Similarity 100.0%;  Pred. No. 7.9e-58;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy 1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

```

Db      2720  |||||CCCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2779
Qy      61   CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
Db      2780  |||||CCCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 2839
Qy      121  GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
Db      2840  |||||GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2899
Qy      181  CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
Db      2900  |||||CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2935

```

RESULT 7

US-10-403-676-19

; Sequence 19, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

```

; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 19
;   LENGTH: 2995
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(2995)
US-10-403-676-19

```

```

Query Match          100.0%; Score 216; DB 12; Length 2995;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      2771 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2830

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          |||
Db      2831 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2890

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      2891 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2950

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      2951 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2986

```

RESULT 8

```

US-10-449-548-19
; Sequence 19, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique

```

```

; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 19
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(2995)
US-10-449-548-19

```

```

Query Match          100.0%;  Score 216;  DB 15;  Length 2995;
Best Local Similarity 100.0%;  Pred. No. 8e-58;
Matches 216;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy          1 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
|
Db          2771 CCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2830
|

Qy          61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
|
Db          2831 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 2890
|

```

Qy 121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
 |||
 Db 2891 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2950
 Qy 181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
 |||
 Db 2951 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2986

RESULT 9

US-10-403-676-27

; Sequence 27, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
 AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

```

; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3055)
US-10-403-676-27

```

```

Query Match          100.0%; Score 216; DB 12; Length 3055;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2831 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2890

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2891 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 2950

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2951 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3010

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
      ||||||||||||||||||||||||||||||||||||
Db      3011 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046

```

RESULT 10

US-10-449-548-27

; Sequence 27, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

```

; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng

```

```

; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
; LENGTH: 3055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3055)
US-10-449-548-27

```

```

Query Match          100.0%; Score 216; DB 15; Length 3055;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          |||
Db      2831 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2890

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          |||
Db      2891 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 2950

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 180
          |||
Db      2951 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCC 3010

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          |||
Db      3011 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046

```

RESULT 11

US-10-403-676-17

; Sequence 17, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187

; PRIOR FILING DATE: 2001-09-19

; PRIOR APPLICATION NUMBER: 60/371,002

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 09/538,092

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 09/604,286

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/140,584

; PRIOR FILING DATE: 1999-06-23


```

; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
; LENGTH: 3106
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3106)
US-10-403-676-17

```

```

Query Match          100.0%; Score 216; DB 12; Length 3106;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCGCCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2882 CCGCCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2941

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2942 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 3001

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3002 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3061

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGGTGTACA 216
          ||||||||||||||||||||||||||||
Db      3062 CTTTCCACATCCATGAAGCCCAATGATGCGGTGTACA 3097

```

RESULT 12

US-10-449-548-17

```

; Sequence 17, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30

```

```

; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
; LENGTH: 3106
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3106)
US-10-449-548-17

```

```

Query Match          100.0%; Score 216; DB 15; Length 3106;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2882 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2941

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2942 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 3001

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3002 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3061

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||||||
Db      3062 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3097

```

```

RESULT 13
US-10-403-676-47
; Sequence 47, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:

```

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-403-676-47

Query Match 100.0%; Score 216; DB 12; Length 3165;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    2938 CCGCCGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2997

Qy     61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCG 120
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Qy    121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3058 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3117

Qy    181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||
Db    3118 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3153
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RESULT 14

US-10-449-548-47

; Sequence 47, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798

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; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
;   LENGTH: 3165
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (13)..(3153)
US-10-449-548-47
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Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      2938 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2997

Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2998 CAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCG 3057

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3058 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3117

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||||||||||
Db      3118 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3153
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RESULT 15

US-09-991-053-5

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; Sequence 5, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: USSN 60/123,667
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; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(2865)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2882)
; OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-5
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Query Match          100.0%; Score 216; DB 10; Length 3333;
Best Local Similarity 100.0%; Pred. No. 8e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 120
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Db      2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCG 3044

Qy      121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3104

Qy      181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
          ||||||||||||||||||||||||||||||||||||
Db      3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140
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Search completed: March 26, 2004, 04:05:56
Job time : 78.6346 secs
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